

**In the specification**

1. Please Amend Table 2B on page 28 as follows:

**Table 2B Polymerase Domain Mutations in Various DNA Polymerases**

Enzyme	Domain (bp)	Domain sequence	Predicted Mutations for Reducing DNA Polymerase Activity#
	<b>DXXSLYP</b>		
Pfu	405-411	DFRALYP	D405 (D405E)
Tgo	404-410	DFRSLYP	D404 (D404E)
KOD	404-410	DFRSLYP	D404 (D404E)
Vent	407-413	DFRSLYP	D407 [(D404E)] <u>D407E</u>
Deep Vent	405-411	DFRSLYP	D405 [(D404E)] <u>D405E</u>
	<b>YXDTDS</b>		
Pfu	539-544	YIDTDG	T542, D543 (T542P; D543G)
Tgo	538-543	YADTDG	T541, D542 (T541P; D542G)
KOD	538-543	YSDDTDG	T541, D542 (T541P; D542G)
Vent	541-546	YADTDG	T544, D545 (T544P; D545G)
Deep Vent	539-544	YIDTDG	T542, D543 (T542P; D543G)
	<b>KXY</b>		
Pfu	593-595	KRY	K593 (K593T)
Tgo	592-594	KKY	K592 (K592T)
KOD	592-594	KKY	K592 (K592T)
Vent	595-597	KRY	K595 (K595T)
Deep			

Vent	593-595	KKY	K593 (K593T)
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2. On page 19, before the full paragraph starting with “Enzymes possessing 3’-5’ exonuclease activity” and ends with “Preferably, the enzyme comprising 3’-5’ exonuclease activity is a DNA polymerase,” please add the following text:

--Amino acid sequence of JDF-3 DNA polymerase (Sequence 2 of WO 01/32887):

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Met Ile Leu Asp Val Asp Tyr Ile Thr Glu Asn Gly Lys Pro Val Ile
1           5           10           15
Arg Val Phe Lys Lys Glu Asn Gly Glu Phe Arg Ile Glu Tyr Asp Arg
           20           25           30
Glu Phe Glu Pro Tyr Phe Tyr Ala Leu Leu Arg Asp Asp Ser Ala Ile
           35           40           45
Glu Glu Ile Lys Lys Ile Thr Ala Glu Arg His Gly Arg Val Val Lys
           50           55           60
Val Lys Arg Ala Glu Lys Val Lys Lys Lys Phe Leu Gly Arg Ser Val
65           70           75           80
Glu Val Trp Val Leu Tyr Phe Thr His Pro Gln Asp Val Pro Ala Ile
           85           90           95
Arg Asp Lys Ile Arg Lys His Pro Ala Val Ile Asp Ile Tyr Glu Tyr
           100          105          110
Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro
           115          120          125
Met Glu Gly Glu Glu Glu Leu Lys Leu Met Ser Phe Asp Ile Glu Thr
           130          135          140
Leu Tyr His Glu Gly Glu Glu Phe Gly Thr Gly Pro Ile Leu Met Ile
145          150          155          160

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Ser	Tyr	Ala	Asp	Glu	Ser	Glu	Ala	Arg	Val	Ile	Thr	Trp	Lys	Lys	Ile
				165					170					175	
Asp	Leu	Pro	Tyr	Val	Glu	Val	Val	Ser	Thr	Glu	Lys	Glu	Met	Ile	Lys
				180					185					190	
Arg	Phe	Leu	Arg	Val	Val	Lys	Glu	Lys	Asp	Pro	Asp	Val	Leu	Ile	Thr
				195					200					205	
Tyr	Asn	Gly	Asp	Asn	Phe	Asp	Phe	Ala	Tyr	Leu	Lys	Lys	Arg	Cys	Glu
				210					215					220	
Lys	Leu	Gly	Val	Ser	Phe	Thr	Leu	Gly	Arg	Asp	Gly	Ser	Glu	Pro	Lys
				225					230					235	
Ile	Gln	Arg	Met	Gly	Asp	Arg	Phe	Ala	Val	Glu	Val	Lys	Gly	Arg	Val
				245					250					255	
His	Phe	Asp	Leu	Tyr	Pro	Val	Ile	Arg	Arg	Thr	Ile	Asn	Leu	Pro	Thr
				260					265					270	
Tyr	Thr	Leu	Glu	Ala	Val	Tyr	Glu	Ala	Val	Phe	Gly	Lys	Pro	Lys	Glu
				275					280					285	
Lys	Val	Tyr	Ala	Glu	Glu	Ile	Ala	Thr	Ala	Trp	Glu	Thr	Gly	Glu	Gly
				290					295					300	
Leu	Glu	Arg	Val	Ala	Arg	Tyr	Ser	Met	Glu	Asp	Ala	Arg	Val	Thr	Tyr
				305					310					315	
Glu	Leu	Gly	Arg	Glu	Phe	Phe	Pro	Met	Glu	Ala	Gln	Leu	Ser	Arg	Leu
				325					330					335	
Ile	Gly	Gln	Gly	Leu	Trp	Asp	Val	Ser	Arg	Ser	Ser	Thr	Gly	Asn	Leu
				340					345					350	
Val	Glu	Trp	Phe	Leu	Leu	Arg	Lys	Ala	Tyr	Glu	Arg	Asn	Glu	Leu	Ala
				355					360					365	

Pro Asn Lys	Pro Asp Glu Arg Glu Leu Ala Arg Arg Arg Gly Gly Tyr
370	375 380
Ala Gly Gly Tyr Val Lys Glu Pro Glu Arg Gly Leu Trp Asp Asn Ile	
385	390 395 400
Val Tyr Leu Asp Phe Arg Ser Leu Tyr Pro Ser Ile Ile Ile Thr His	
405	410 415
Asn Val Ser Pro Asp Thr Leu Asn Arg Glu Gly Cys Arg Ser Tyr Asp	
420	425 430
Val Ala Pro Glu Val Gly His Lys Phe Cys Lys Asp Phe Pro Gly Phe	
435	440 445
Ile Pro Ser Leu Leu Gly Asn Leu Leu Glu Glu Arg Gln Lys Ile Lys	
450	455 460
Arg Lys Met Lys Ala Thr Leu Asp Pro Leu Glu Lys Asn Leu Leu Asp	
465	470 475 480
Tyr Arg Gln Arg Ala Ile Lys Ile Leu Ala Asn Ser Tyr Tyr Gly Tyr	
485	490 495
Tyr Gly Tyr Ala Arg Ala Arg Trp Tyr Cys Arg Glu Cys Ala Glu Ser	
500	505 510
Val Thr Ala Trp Gly Arg Glu Tyr Ile Glu Met Val Ile Arg Glu Leu	
515	520 525
Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ala Asp Thr Asp Gly Leu	
530	535 540
His Ala Thr Ile Pro Gly Ala Asp Ala Glu Thr Val Lys Lys Lys Ala	
545	550 555 560
Met Glu Phe Leu Asn Tyr Ile Asn Pro Lys Leu Pro Gly Leu Leu Glu	
565	570 575
Leu Glu Tyr Glu Gly Phe Tyr Val Arg Gly Phe Phe Val Thr Lys Lys	

580	585	590	
Lys Tyr Ala Val Ile Asp Glu Glu Gly Lys Ile Thr Thr Arg Gly Leu			
595	600	605	
Glu Ile Val Arg Arg Asp Trp Ser Glu Ile Ala Lys Glu Thr Gln Ala			
610	615	620	
Arg Val Leu Glu Ala Ile Leu Arg His Gly Asp Val Glu Glu Ala Val			
625	630	635	640
Arg Ile Val Arg Glu Val Thr Glu Lys Leu Ser Lys Tyr Glu Val Pro			
645	650	655	
Pro Glu Lys Leu Val Ile His Glu Gln Ile Thr Arg Glu Leu Lys Asp			
660	665	670	
Tyr Lys Ala Thr Gly Pro His Val Ala Ile Ala Lys Arg Leu Ala Ala			
675	680	685	
Arg Gly Val Lys Ile Arg Pro Gly Thr Val Ile Ser Tyr Ile Val Leu			
690	695	700	
Lys Gly Ser Gly Arg Ile Gly Asp Arg Ala Ile Pro Phe Asp Glu Phe			
705	710	715	720
Asp Pro Thr Lys His Lys Tyr Asp Ala Asp Tyr Tyr Ile Glu Asn Gln			
725	730	735	
Val Leu Pro Ala Val Glu Arg Ile Leu Arg Ala Phe Gly Tyr Arg Lys			
740	745	750	
Glu Asp Leu Arg Tyr Gln Lys Thr Arg Gln Val Gly Leu Gly Ala Trp			
755	760	765	
Leu Lys Pro Lys Gly Lys Lys Lys (SEQ ID NO: 10)			
770	775		

## --Nucleotide sequence of JDF-3 DNA polymerase (Sequence 1 of WO 01/32887)

atgatccttg acgttgatta catcaccgag aatggaaagc ccgtcatcag ggtcttcaag	60
aaggagaacg gcgagttcag gattgaatac gaccgcgagt tcgagcccta cttctacgcg	120
ctcctcaggg acgactctgc catcgaagaa atcaaaaaga taaccgcgga gaggcacggc	180
agggctcgta aggttaagcg cgcggagaag gtgaagaaaa agttcctcgg caggtctgtg	240
gaggtctggg tcctctactt cacgcacccg caggacgttc cggcaatccg cgacaaaata	300
aggaagcacc ccgcggtcat cgacatctac gagtacgaca tacccttcgc caagcgctac	360
ctcatagaca agggcctaata cccgatggaa ggtgaggaag agcttaaact catgtccttc	420
gacatcgaga cgctctacca cgagggagaa gagtttgaa cggggccgat tctgatgata	480
agctacgccg atgaaagcga ggcgcgctg ataacctgga agaagatcga ccttccttac	540
gttgaggttg tctccaccga gaaggagatg attaagcgct tcttgagggt cgtaaggag	600
aaggaccgg acgtgctgat aacatacaac ggcgacaact tcgacttcgc ctacctgaaa	660
aagcgctgtg agaagcttgg cgtgagcttt accctcggga gggacgggag cgagccgaag	720
atacagcgca tgggggacag gtttgcggtc gaggtgaagg gcagggtaca cttcgacctt	780
tatccagtca taaggcgcac cataaacctc ccgacctaca cccttgaggc tgtatacgag	840
gcggttttcg gcaagcccaa ggagaaggtc tacgccgagg agatagccac cgctggggag	900
accggcgagg ggcttgagag ggtcgcgcgc tactcgatgg aggacgcgag ggttacctac	960
gagcttgga gggagttctt cccgatggag gccagcttt ccaggctcat cggccaaggc	1020
ctctgggacg tttcccgtc cagcaccggc aacctcgtcg agtggttcct cctaaggaag	1080
gcctacgaga ggaacgaact cgctcccaac aagcccgcg agaggagct ggcgaggaga	1140
agggggggct acgccggtgg ctacgtcaag gagccggagc ggggactgtg ggacaatatc	1200
gtgtatctag actttcgtag tctctaccct tcaatcataa tcaccacaa cgtctcgcca	1260
gatacgctca accgcgaggg gtgtaggagc tacgacgttg ccccgagggt cggtcacaag	1320
ttctgcaagg acttccccgg cttcattccg agcctgctcg gaaacctgct ggaggaaaagg	1380
cagaagataa agaggaagat gaaggcaact ctcgacccgc tggagaagaa tctcctcgat	1440
tacaggcaac gcgccatcaa gattctcgcc aacagctact acggctacta cggctatgcc	1500
agggcaagat ggtactgcag ggagtgcgcc gagagcgta cggcatgggg aagggagtac	1560

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atcgaaatgg tcatcagaga gcttgaggaa aagttcgggt ttaaagtcct ctatgcagac 1620
acagacgggtc tccatgccac cattcctgga gcggacgctg aaacagtcaa gaaaaaggca 1680
atggagttct taaactatat caatcccaaa ctgcccggcc ttctcgaact cgaatacgag 1740
ggcttctacg tcaggggctt cttcgtcacg aagaaaaagt acgcgggtcat cgacgaggag 1800
ggcaagataa ccacgcgcgg gcttgagata gtcaggcgcg actggagcga gatagcgaag 1860
gagacgcagg cgaggggttt ggaggcgata ctcaggcacg gtgacgttga agaggccgtc 1920
agaattgtca ggaagtcac cgaaaagctg agcaagtacg aggttccgcc ggagaagctg 1980
gttatccacg agcagataac gcgcgagctc aaggactaca aggccaccgg cccgcacgta 2040
gccatagcga agcgtttggc cgccagaggt gttaaaatcc ggcccggaac tgtgataagc 2100
tacatcgttc tgaagggtc cggaaggata ggcgacaggg cgattccctt cgacgagttc 2160
gacccgacga agcacaagta cgatgcggac tactacatcg agaaccaggt tctgccggca 2220
gttgagagaa tcctcagggc cttcggctac cgcaaggaag acctgcgcta ccagaagacg 2280
aggcaggtcg ggcttggcgc gtggctgaag ccgaagggga agaagaagtg a 2331 (SEQ ID NO: 11)
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